AMENDMENT TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

1. (Currently amended) A method for identification of a pathogenic organism from a predetermined group of pathogens, comprising:
   a) at least partially purifying nucleic acid from a clinical sample to create a clinical specimen,
   b) subjecting at least a first aliquot of said clinical specimen to at least a first ~~one~~ amplification and detection reaction in one reaction vessel comprising:
      ba) an amplification step using at least a first set of amplification primers capable of amplifying a pre-selected nucleic acid sequence comprising the 16s/23s or 18s/26s rRNA spacer region from several or all members of said predetermined group of pathogens, and
      bb) a detection step using a plurality of hybridization reagents, said reagents together being capable of specifically detecting a pre-selected nucleic acid sequence comprising the 16s/23s or 18s/26s rRNA spacer region from all members of said group of pathogens, said detection step ~~bb)~~ comprising:
         bba) monitoring hybridization of each of said hybridization reagents at a pre-selected temperature, said hybridization being indicative of at least the genus of said pathogen present in the sample, and
         bbb) monitoring temperature dependence of hybridization, said temperature dependence being indicative of at least the species of said pathogen, ~~determining whether said amplification and detection reaction is indicative for the presence of a specific member of said pre-selected group of pathogens.~~

   wherein said amplification and detection reaction is indicative of the identity of said pathogenic organism from a predetermined group of pathogens.

2. ~~2.~~ (Currently amended) Method according to claim 1, further comprising subjecting ~~wherein a first and~~ at least a second aliquot of said clinical specimen ~~each are subjected~~ to

~~an~~ at least a second amplification and detection reaction in a different reaction vessel from ~~independently from each other~~ said first aliquot of said clinical specimen being subjected to said first amplification and detection reaction. ~~in two different reaction vessels.~~

3. (Currently amended) Method according to claim 2, further comprising subjecting ~~wherein a first, a second and~~ at least a third aliquot of said clinical specimen ~~each are subjected~~ to ~~an~~ at least a third amplification and detection reaction in a different reaction vessel from ~~independently from each other~~ said first aliquot of said clinical specimen being subjected to said first amplification and detection reaction, and said second aliquot of said clinical specimen being subjected to said second amplification and detection reaction. ~~in two different reaction vessels.~~

4. (Currently amended) Method according to claim 1, further comprising ~~wherein an additional~~ a hybridization reagent ~~is used for the detection of~~ capable of specifically detecting an internal control.

5. (Currently amended) Method according to claim 2, wherein gram positive pathogenic organisms are exclusively identified by said first ~~the other~~ amplification and detection reaction, and gram negative pathogenic organisms are exclusively identified by said second ~~the amount~~ amplification and detection reaction.

6. (Currently amended) Method according to claim 3, wherein fungal pathogens are exclusively identified in said ~~the~~ third amplification and detection reaction.

7. (Currently amended) Method according to ~~claims~~ claim 2, wherein said first amplification and detection reaction and said second ~~each~~ amplification and detection reaction ~~step is~~ are performed with the same thermocycling profile.

8. – 9. (Canceled)